



IFWO

RAW SEQUENCE LISTING

DATE: 05/25/2004

PATENT APPLICATION: US/10/849,106

TIME: 08:04:06

Input Set : N:\CrF3\RULE60\10849106.raw

Output Set: N:\CRF4\05252004\J849106.raw

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1 <110> APPLICANT: Udagawa, Hiroaki
2   Frandsen, Torben
3   Nielsen, Tom
4   Kauppinen, Markus
5   Christensen, Soeren
6 <120> TITLE OF INVENTION: Lysophospholipase
7 <130> FILE REFERENCE: 5958.210-US
8 <140> CURRENT APPLICATION NUMBER: US/10/849,106
9 <141> CURRENT FILING DATE: 2004-05-19
10 <150> PRIOR APPLICATION NUMBER: US/09/687,538
11 <151> PRIOR FILING DATE: 2000-10-13
12 <160> NUMBER OF SEQ ID NOS: 19
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 1923
17 <212> TYPE: DNA
18 <213> ORGANISM: Aspergillus niger
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21 <222> LOCATION: (1)..(1920)
22 <223> OTHER INFORMATION:
23 <221> NAME/KEY: sig_peptide
24 <222> LOCATION: (1)..(63)
25 <223> OTHER INFORMATION:
W--> 26 <221> mat_peptide
27 <222> LOCATION: (109)..()
28 <223> OTHER INFORMATION:
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30   atg aag ttc aat gca ctc tta acg acc ctc gcg gcg ctg ggg tat atc      48
31   Met Lys Phe Asn Ala Leu Leu Thr Thr Leu Ala Ala Leu Gly Tyr Ile
32   -35                    -30                    -25
33   caa gga ggc gcc gcg gtt cct aca acc gtc gac ctc aca tat gca gac      96
34   Gln Gly Gly Ala Ala Val Pro Thr Thr Val Asp Leu Thr Tyr Ala Asp
35   -20                    -15                    -10                    -5
36   ata tca cct cgc gca ctg gat aat gcc cct gat ggt tat acc ccg agc      144
37   Ile Ser Pro Arg Ala Leu Asp Asn Ala Pro Asp Gly Tyr Thr Pro Ser
38   -1  1                    5                    10
39   aat gta tcc tgt cct gca aac aga ccg acg att cgc agc gcg tca acc      192
40   Asn Val Ser Cys Pro Ala Asn Arg Pro Thr Ile Arg Ser Ala Ser Thr
41   15                    20                    25
42   ctg tca tcg aac gag acg gca tgg gtg gac gtc cgg cgt aag cag act      240
43   Leu Ser Ser Asn Glu Thr Ala Trp Val Asp Val Arg Arg Lys Gln Thr
44   30                    35                    40

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45	gtc tca gcg atg aaa gac ctt ttc ggc cat atc aac atg agc tca ttt	288
46	Val Ser Ala Met Lys Asp Leu Phe Gly His Ile Asn Met Ser Ser Phe	
47	45 50 55 60	
48	gac gct att tcg tac atc aac agc cat tca aat atc acc aac ata	336
49	Asp Ala Ile Ser Tyr Ile Asn Ser His Ser Ser Asn Ile Thr Asn Ile	
50	65 70 75	
51	ccc aac atc ggt att gcc gtg tcc ggc ggt ggc tac aga gcc ctg acc	384
52	Pro Asn Ile Gly Ile Ala Val Ser Gly Gly Gly Tyr Arg Ala Leu Thr	
53	80 85 90	
54	aac ggc gcg gga gca ctc aag gca ttc gac agt cga acg gaa aac tca	432
55	Asn Gly Ala Gly Ala Leu Lys Ala Phe Asp Ser Arg Thr Glu Asn Ser	
56	95 100 105	
57	acc cat aat gga cag ctc ggt ggt ctt ctg cag tca gcc aca tac ctg	480
58	Thr His Asn Gly Gln Leu Gly Gly Leu Leu Gln Ser Ala Thr Tyr Leu	
59	110 115 120	
60	tcc ggt ctc tcc gga ggt ggc tgg ctc ctg ggc tca atc tac atc aac	528
61	Ser Gly Leu Ser Gly Gly Gly Trp Leu Leu Gly Ser Ile Tyr Ile Asn	
62	125 130 135 140	
63	aac ttc acc acc gtc tcc aat ctg caa acc tac aaa gag ggc gaa gtc	576
64	Asn Phe Thr Thr Val Ser Asn Leu Gln Thr Tyr Lys Glu Gly Glu Val	
65	145 150 155	
66	tgg cag ttc cag aat tca atc acg aaa ggc cca aag acc aac ggc ttg	624
67	Trp Gln Phe Gln Asn Ser Ile Thr Lys Gly Pro Lys Thr Asn Gly Leu	
68	160 165 170	
69	caa gct tgg gat aca gcc aag tac tac cgc gat ctg gcc aag gtg gtc	672
70	Gln Ala Trp Asp Thr Ala Lys Tyr Tyr Arg Asp Leu Ala Lys Val Val	
71	175 180 185	
72	gct ggc aag aag gac gcg ggc ttc aac act tcc ttc acg gac tac tgg	720
73	Ala Gly Lys Lys Asp Ala Gly Phe Asn Thr Ser Phe Thr Asp Tyr Trp	
74	190 195 200	
75	ggt cgc gca ctc tcc tac cag ctg att aac gcg acc gac gga ggc cca	768
76	Gly Arg Ala Leu Ser Tyr Gln Leu Ile Asn Ala Thr Asp Gly Gly Pro	
77	205 210 215 220	
78	ggc tac acc tgg tca tcg atc gct tta acc cag ggc ttc aag aac gga	816
79	Gly Tyr Thr Trp Ser Ser Ile Ala Leu Thr Gln Gly Phe Lys Asn Gly	
80	225 230 235	
81	aac atg ccc atg ccg ctc ctt gtc gcc gac ggc cgc aac cca ggc gag	864
82	Asn Met Pro Met Pro Leu Leu Val Ala Asp Gly Arg Asn Pro Gly Glu	
83	240 245 250	
84	acc cta atc ggc agc aac tcg acc gtg tat gag ttc aac ccc tgg gaa	912
85	Thr Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn Pro Trp Glu	
86	255 260 265	
87	ttc ggc agt ttt gat ccg tcc atc ttc ggc ttc gct ccc ctc gaa tac	960
88	Phe Gly Ser Phe Asp Pro Ser Ile Phe Gly Phe Ala Pro Leu Glu Tyr	
89	270 275 280	
90	ctc gga tcc tac ttt gag aac ggc gaa gtc cca tcc agc cga tcc tgc	1008
91	Leu Gly Ser Tyr Phe Glu Asn Gly Glu Val Pro Ser Ser Arg Ser Cys	
92	285 290 295 300	
93	gtc cgc ggc ttc gat aac gca ggc ttc gtc atg gga acc tcc tcc agt	1056

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94 Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr Ser Ser Ser
95                               305                               310                               315
96 ctc ttc aac caa ttc atc ctg aag ctc aac acc acc gac atc cca tca      1104
97 Leu Phe Asn Gln Phe Ile Leu Lys Leu Asn Thr Thr Asp Ile Pro Ser
98                               320                               325                               330
99 acc ctc aaa acg gtc atc gcc agc atc cta gaa gaa cta ggc gac cgc      1152
100 Thr Leu Lys Thr Val Ile Ala Ser Ile Leu Glu Glu Leu Gly Asp Arg
101                               335                               340                               345
102 aac gac gac atc gcc atc tac tct ccc aac ccc ttc tac ggg tac cgc      1200
103 Asn Asp Asp Ile Ala Ile Tyr Ser Pro Asn Pro Phe Tyr Gly Tyr Arg
104                               350                               355                               360
105 aac gcg aca gtt tca tac gaa aag acc ccg gac ctg aac gtc gtc gac      1248
106 Asn Ala Thr Val Ser Tyr Glu Lys Thr Pro Asp Leu Asn Val Val Asp
107                               365                               370                               375                               380
108 ggt ggc gaa gac aaa cag aac ctc ccc ctc cat cct ctc atc caa ccc      1296
109 Gly Gly Glu Asp Lys Gln Asn Leu Pro Leu His Pro Leu Ile Gln Pro
110                               385                               390                               395
111 gcc cgc aac gtg gac gtc atc ttc gcc gtc gac tcc tca gcc agt acc      1344
112 Ala Arg Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser Ala Ser Thr
113                               400                               405                               410
114 tcg gac aac tgg ccc aac gga agt cct ctc gtc gcg act tac gaa cgt      1392
115 Ser Asp Asn Trp Pro Asn Gly Ser Pro Leu Val Ala Thr Tyr Glu Arg
116                               415                               420                               425
117 agt ctc aac tca acc ggt atc gga aac ggc acc gcg ttc cct agc atc      1440
118 Ser Leu Asn Ser Thr Gly Ile Gly Asn Gly Thr Ala Phe Pro Ser Ile
119                               430                               435                               440
120 ccg gac aag agc acc ttc att aac ctg ggc ttg aac acc cgt ccg act      1488
121 Pro Asp Lys Ser Thr Phe Ile Asn Leu Gly Leu Asn Thr Arg Pro Thr
122                               445                               450                               455                               460
123 ttc ttc ggc tgc aat agt tcc aat atc aca ggc cat gca ccc ctg gtt      1536
124 Phe Phe Gly Cys Asn Ser Ser Asn Ile Thr Gly His Ala Pro Leu Val
125                               465                               470                               475
126 gtc tac ctc ccc aac tac ccc tac aca acc ctc tcc aac aag tcg acc      1584
127 Val Tyr Leu Pro Asn Tyr Pro Tyr Thr Thr Leu Ser Asn Lys Ser Thr
128                               480                               485                               490
129 ttc cag ctc aag tac gag atc ttg gag cgt gat gag atg atc acc aat      1632
130 Phe Gln Leu Lys Tyr Glu Ile Leu Glu Arg Asp Glu Met Ile Thr Asn
131                               495                               500                               505
132 ggc tgg aac gtg gtt act atg ggt aat gga tca agg aag tct tac gag      1680
133 Gly Trp Asn Val Val Thr Met Gly Asn Gly Ser Arg Lys Ser Tyr Glu
134                               510                               515                               520
135 gat tgg ccg act tgt gcg ggc tgc gct att ctg agt cgc tcg ttt gat      1728
136 Asp Trp Pro Thr Cys Ala Gly Cys Ala Ile Leu Ser Arg Ser Phe Asp
137                               525                               530                               535                               540
138 ccg act aat acc cag gtg ccg gat atg tgc tcg cag tgt ttt gac aag      1776
139 Arg Thr Asn Thr Gln Val Pro Asp Met Cys Ser Gln Cys Phe Asp Lys
140                               545                               550                               555
141 tat tgc tgg gat gga acg agg aat agt acg acg ccg gcg gcg tat gag      1824
142 Tyr Cys Trp Asp Gly Thr Arg Asn Ser Thr Thr Pro Ala Ala Tyr Glu

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143          560          565          570
144  ccg aag gta ttg atg gct agt gcg ggt gtg agg ggt att tcg atg tcg      1872
145  Pro Lys Val Leu Met Ala Ser Ala Gly Val Arg Gly Ile Ser Met Ser
146          575          580          585
147  agg ttg gtt ttg ggt ctc ttt ccg gtg gtg gtt ggg gtt tgg atg atg      1920
148  Arg Leu Val Leu Gly Leu Phe Pro Val Val Val Gly Val Trp Met Met
149          590          595          600
150  tga      1923
152 <210> SEQ ID NO: 2
153 <211> LENGTH: 640
154 <212> TYPE: PRT
155 <213> ORGANISM: Aspergillus niger
156 <400> SEQUENCE: 2
157  Met Lys Phe Asn Ala Leu Leu Thr Thr Leu Ala Ala Leu Gly Tyr Ile
158      -35          -30          -25
159  Gln Gly Gly Ala Ala Val Pro Thr Thr Val Asp Leu Thr Tyr Ala Asp
160      -20          -15          -10          -5
161  Ile Ser Pro Arg Ala Leu Asp Asn Ala Pro Asp Gly Tyr Thr Pro Ser
162          -1  1          5          10
163  Asn Val Ser Cys Pro Ala Asn Arg Pro Thr Ile Arg Ser Ala Ser Thr
164          15          20          25
165  Leu Ser Ser Asn Glu Thr Ala Trp Val Asp Val Arg Arg Lys Gln Thr
166          30          35          40
167  Val Ser Ala Met Lys Asp Leu Phe Gly His Ile Asn Met Ser Ser Phe
168          45          50          55          60
169  Asp Ala Ile Ser Tyr Ile Asn Ser His Ser Ser Asn Ile Thr Asn Ile
170          65          70          75
171  Pro Asn Ile Gly Ile Ala Val Ser Gly Gly Gly Tyr Arg Ala Leu Thr
172          80          85          90
173  Asn Gly Ala Gly Ala Leu Lys Ala Phe Asp Ser Arg Thr Glu Asn Ser
174          95          100          105
175  Thr His Asn Gly Gln Leu Gly Gly Leu Leu Gln Ser Ala Thr Tyr Leu
176          110          115          120
177  Ser Gly Leu Ser Gly Gly Gly Trp Leu Leu Gly Ser Ile Tyr Ile Asn
178          125          130          135          140
179  Asn Phe Thr Thr Val Ser Asn Leu Gln Thr Tyr Lys Glu Gly Glu Val
180          145          150          155
181  Trp Gln Phe Gln Asn Ser Ile Thr Lys Gly Pro Lys Thr Asn Gly Leu
182          160          165          170
183  Gln Ala Trp Asp Thr Ala Lys Tyr Tyr Arg Asp Leu Ala Lys Val Val
184          175          180          185
185  Ala Gly Lys Lys Asp Ala Gly Phe Asn Thr Ser Phe Thr Asp Tyr Trp
186          190          195          200
187  Gly Arg Ala Leu Ser Tyr Gln Leu Ile Asn Ala Thr Asp Gly Gly Pro
188          205          210          215          220
189  Gly Tyr Thr Trp Ser Ser Ile Ala Leu Thr Gln Gly Phe Lys Asn Gly
190          225          230          235
191  Asn Met Pro Met Pro Leu Leu Val Ala Asp Gly Arg Asn Pro Gly Glu
192          240          245          250

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193 Thr Leu Ile Gly Ser Asn Ser Thr Val Tyr Glu Phe Asn Pro Trp Glu
194           255           260           265
195 Phe Gly Ser Phe Asp Pro Ser Ile Phe Gly Phe Ala Pro Leu Glu Tyr
196           270           275           280
197 Leu Gly Ser Tyr Phe Glu Asn Gly Glu Val Pro Ser Ser Arg Ser Cys
198           285           290           295           300
199 Val Arg Gly Phe Asp Asn Ala Gly Phe Val Met Gly Thr Ser Ser Ser
200           305           310           315
201 Leu Phe Asn Gln Phe Ile Leu Lys Leu Asn Thr Thr Asp Ile Pro Ser
202           320           325           330
203 Thr Leu Lys Thr Val Ile Ala Ser Ile Leu Glu Glu Leu Gly Asp Arg
204           335           340           345
205 Asn Asp Asp Ile Ala Ile Tyr Ser Pro Asn Pro Phe Tyr Gly Tyr Arg
206           350           355           360
207 Asn Ala Thr Val Ser Tyr Glu Lys Thr Pro Asp Leu Asn Val Val Asp
208           365           370           375           380
209 Gly Gly Glu Asp Lys Gln Asn Leu Pro Leu His Pro Leu Ile Gln Pro
210           385           390           395
211 Ala Arg Asn Val Asp Val Ile Phe Ala Val Asp Ser Ser Ala Ser Thr
212           400           405           410
213 Ser Asp Asn Trp Pro Asn Gly Ser Pro Leu Val Ala Thr Tyr Glu Arg
214           415           420           425
215 Ser Leu Asn Ser Thr Gly Ile Gly Asn Gly Thr Ala Phe Pro Ser Ile
216           430           435           440
217 Pro Asp Lys Ser Thr Phe Ile Asn Leu Gly Leu Asn Thr Arg Pro Thr
218           445           450           455           460
219 Phe Phe Gly Cys Asn Ser Ser Asn Ile Thr Gly His Ala Pro Leu Val
220           465           470           475
221 Val Tyr Leu Pro Asn Tyr Pro Tyr Thr Thr Leu Ser Asn Lys Ser Thr
222           480           485           490
223 Phe Gln Leu Lys Tyr Glu Ile Leu Glu Arg Asp Glu Met Ile Thr Asn
224           495           500           505
225 Gly Trp Asn Val Val Thr Met Gly Asn Gly Ser Arg Lys Ser Tyr Glu
226           510           515           520
227 Asp Trp Pro Thr Cys Ala Gly Cys Ala Ile Leu Ser Arg Ser Phe Asp
228           525           530           535           540
229 Arg Thr Asn Thr Gln Val Pro Asp Met Cys Ser Gln Cys Phe Asp Lys
230           545           550           555
231 Tyr Cys Trp Asp Gly Thr Arg Asn Ser Thr Thr Pro Ala Ala Tyr Glu
232           560           565           570
233 Pro Lys Val Leu Met Ala Ser Ala Gly Val Arg Gly Ile Ser Met Ser
234           575           580           585
235 Arg Leu Val Leu Gly Leu Phe Pro Val Val Val Gly Val Trp Met Met
236           590           595           600
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 1917
240 <212> TYPE: DNA
241 <213> ORGANISM: Aspergillus niger
242 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/849,106

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Input Set : N:\Crf3\RULE60\10849106.raw
Output Set: N:\CRF4\05252004\J849106.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9

Seq#:13; N Pos: 3,6,9,15,18,24

Seq#:14; N Pos. 16,19

VERIFICATION SUMMARY

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Input Set : N:\Crif3\RULE60\10849106.raw

Output Set: N:\CRF4\05252004\J849106.raw

L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:249 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:468 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:468 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:471 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:471 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:471 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:688 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:911 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:914 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:916 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:925 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:927 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:936 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:938 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:947 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:949 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:958 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:961 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:964 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:967 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:970 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:973 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:976 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:978 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:987 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:990 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:993 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:995 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1004 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1006 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:1015 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1017 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1026 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1028 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:1037 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1039 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18

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